A. BINDING OF gp120

B. BINDING OF HIV-1

FIG. 1

FIG. 2

SELECTED PREFERENCES:

FIG. 3A

FIG. 3B

FIG. 4

FIG. 5

FIG. 6

FIG. 7

B. LIGAND BLOTTING

5(KψPR)-TASP
5(QPQ)-TASP
NONE

200 –
97 –
68 –
43 –

1   2   3

← 95 kDa

A. CELL SURFACE 125I-LABELING

5(KψPR)-TASP
5(QPQ)-TASP
NONE

200 –
97 –
68 –
43 –

1   2   3
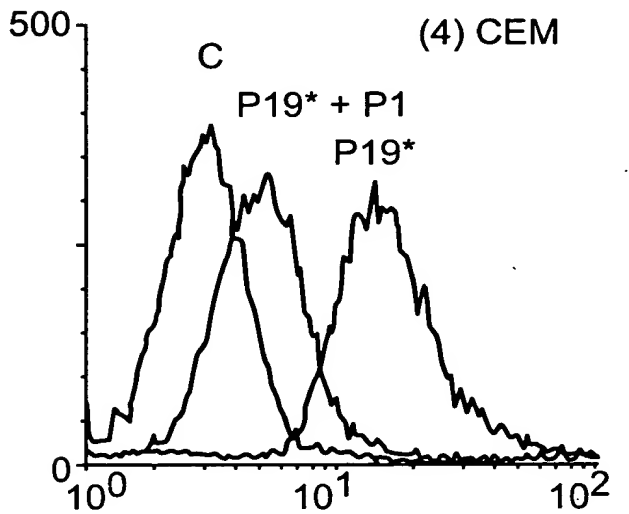
← p95

FIG. 8A

FIG. 8B

FIG. 9

FIG. 10

FIG. 11

1st

A   200 -

97 -

68 -

B   200 -

97 -

68 -

C   200 -

97 -

68 -

2nd

2nd

2nd

4   5   6   7   : pH

FIG. 12

FIG. 13A

FIG. 13B

A.

B.

FIG. 14

FIG. 15

A.

5 DAYS p.i.

CONTROL

C-IgG

α-NUCLEOLIN

α-PHAP II

α-PHAP I

0   50   100   150

HIV PRODUCTION; p24 ng/ml

B.

6 DAYS p.i.

CONTROL

C-IgG

α-NUCLEOLIN

α-PHAP II

α-PHAP I

0   200   400   600

HIV PRODUCTION; p24 ng/ml

FIG. 16

HIV BINDING; p24 pg/ml

FIG. 17

FIG. 18

A. 5[K Ψ(CH$_2$N)PR] -TASP BINDING TO THE V3 LOOP-BPs

B. gp120 BINDING TO THE V3 LOOP-BPs

C. gp120 BINDING TO THE V3 LOOP-BPs

FIG. 19

FIG. 20

FIG. 21

FIG. 22

FIG. 23

FIG. 24

A.

B.

C.

HIV PRODUCTION; p24 ng/ml

FIG. 25

FIG. 26

FIG. 27

FIG. 28

HIV-1 Ba-L

HIV-1 AZT RESISTANT

HIV-1 SAQUINAVIR RESISTANT

HIV-1 NEVIRAPINE RESISTANT

β-GALACTOSIDASE ACTIVITY (OD)

β-GALACTOSIDASE ACTIVITY (OD)

FIG. 29

FIG. 30

FIG. 31

FIG. 32

FIG. 33

FIG. 34

CELL-SURFACE

0   0.1   1   10

CYTOPLASM

0   0.1   1   10   μM

200 -

97 -

68 -

43 -

30 -

-NUCLEOLIN

FIG. 35

CELL-SURFACE

1   2   3   4

-NUCLEOLIN (p95)

1: 1hr; 2: 1hr; 3: 6hr; 4: 24hr;
2, 3, 4: 5μM

FIG. 36

THE EFFECT OF HEPARIN AT µg/ml ON HIV INFECTION IN HeLa P4-C5 CELLS.

FIG. 37

FIG. 38

FIG. 39

FIG. 40A

FIG. 40B

FIG. 41A

FIG. 41B

46/70

RELATIVE CELL NUMBER

AUTO

P19* + P19

P19*

30

20

10

1

LOG FLUORESCENCE INTENSITY

10^0 10^1 10^2 10^3 10^4

FIG. 42A

RELATIVE CELL NUMBER

AUTO

IgG CONTROL

ANTI - p95

20

15

10

5

0

LOG FLUORESCENCE INTENSITY

10^0 10^1 10^2 10^3 10^4

FIG. 42B

RELATIVE CELL NUMBER

AUTO

IgG CONTROL

ANTI - p40

ANTI - p30

120

100

80

60

40

20

0

LOG FLUORESCENCE INTENSITY

10^0 10^1 10^2 10^3 10^4

FIG. 42C

FIG. 43

FIG. 44

FIG. 45

FIG. 46A

FIG. 46B

FIG. 47

FIG. 48

I. (SEQ ID NO: 22)

/translation="MVKLAKAGKNQGDPKKMAPPPKEVEEDSEDEEMSEDEEDDSSGE
EVVIPQKKGKKAAATSAKKVVVSPTKKVAVATPAKKAAVTPGKKAAATPAKKTVTPAK
AVTTPGKKGATPGKALVATPGKKGAAIPAKGAKNGKNAKKEDSDEEEDDDSEEDEEDD
EDEDEDEDEIEPAAMKAAAAAPASEDEDDEDDEDDEDDDDDEEDDSEEEAMETTPAKG
KKAAKVVPVKAKNVAEDEDEEEDDEDEDDDDDEDDEDDDDEDDEEEEEEEEEEPVKEA
PGKRKKEMAKQKAAPEAKKQKVEGTEPTTAFNLFVGNLNFNKSAPELKTGISDVFAKN
DLAVVDVRIGMTRKFGYVDFESAEDLEKALELTGLKVFGNEIKLEKPKGKDSKKERDA
RTLLAKNLPYKVTQDELKEVFEDAAEIRLVSKDGKSKGIAYIEFKTEADAEKTFEEKQ
GTEIDGRSISLYYTGEKGQNQDYRGGKNSTWSGESKTLVLSNLSYSATEETLQEVFEK
ATFIKVPQNQNGKSKGYAFIEFASFEDAKEALNSCNKREIEGRAIRLELQGPRGSPNA
RSQPSKTLFVKGLSEDTTEETLKESFDGSVRARIVTDRETGSSKGFGFVDFNSEEDAK
EAMEDGEIDGNKVTLDWAKPKGEGGFGGRGGGRGGFGGRGGGRGGRGGFGGRGRGGFG
GRGGFRGGRGGGGDHKPQGKKTKFE"
(SEQ ID NO: 23)

II.   1 ATTCTGCTGT AGACATAGAG ATGATGATCA TAGCTGACTA TGATGATGAT

      51 CCCCCGCGAG CCTGAAAGAG GAAATGCTCT GGTTTGCTAA GCCCGCGAAT

     101 CGAGTGAGAC CCACCCACAA AGCTAACCGT GGAAGTCACT GGCGGCCTCC

     151 TTCGCCCTGC CAGCCGGGGA ACCCATCCGG TGGCTCTCGA CCTGCTCCCG

     201 GGCCATCTGG TGACACTGAC TTCGCAGCCA CCACCTTAAT TGGCGCATTC

     251 GACCCAAATA ATAACCTGGG AACCTGTGGG CGGTCTAAGG CCCGGCTCTG

     301 CGGTCGCCCT CCCAGGCCCC TCTCCCTGGC CCTGTGAGGC CAGAAAGTTA

     351 CTTCTCCGAG GCCAGTTCCC CATGTCTGAG AAATATCTCC CAACTTGAGG

     401 TTCTGTGGGG TAGGGGAGGG TTCGTGACTT TCTCACAGAA AACCTCGTAC

FIG. 49

451 AGACCCCGCC ACTGCCTTTA TTAACAGCTC TCAGGAGACT GCCTGCAGGA

501 GGGGGGTCGC TCCGGCCCCA TGCTCGCGGG CAAGCAGGGA TAAGCTGTGC

551 CTCCAAAAGG GCCAACGGGA ACTCCGCGGT CCCTGAACTT CCGGTGCTGG

601 AGGACTCCTC GCTCCAGGGC CACCAGGAGC CGCGGCGTGA GTGCGTGCCG

651 GAACCGAGGG CGGGGTCTCT GAGGAACTCC AAGGCTGCCC AAGCCTACGG

701 ACCCAGCCAC ATTGGCGAAC CGGAGACCGC CCGATTCCAC CACCCCCGCG

751 CTCCCCTCAC AGCCGGCGCC AAAAACGCCA GTCCCACGAC GCAGGCCGGG

801 ACCCGCGCGC CCACGGCCCA ATCAGCGCGA CCTTGCACAA AGCGAGCCCC

851 GCCCCCACGG CGCCGTTGCC AGCCCCTCCC CCTCCCGTGC CGCCTCGGCC

901 CGCCTACTCC CCGCCCCGCG CCGTTCACGG TTAGAGGCTC GCGATTGGCT

951 CATGGGGACG GCCGCGAGCT TTGGTTGGTC GGCGCGGAGT CACGAGGCGC

1001 CGTCGTCGCC TTTCCACAGG CGTTACTGGG CAGGCTCAGT CTTTCGCCTC

1051 AGTCTCGAGC TCTCGCTGGC TTCGGGTGTA CGTGCTCCGG GATCTTCAGC

1101 ACCCGCGGCC GCCATCGCCG TCGCTTGGCT TCTTCTGGAC TCATCTGCGC

1151 CACTTGTCCG CTTCACACTC CGCCGCCATC ATGGTGAAGC TCGCGAAGGT

1201 AAACGGCCTT GAGCGCGACG CAGACGTGTA GGCCTGCTTC CGAGGGGCGA

1251 GCGCGGCGCC GCGGGGAGGA GGGCCTGCGC GCAGTCCCGG GCGCGTTCTA

1301 GGGCGCCATG CTGCGGGAAG TCTCGCGCGA TTAGTGGGGA GGTCTCGCGC

FIG. 49 (CONT. 1)

1351 TTCTGGCTAC TTGGTGGCGA GGTGAAGAGC TTCTGCAGGT GCTGGGGGAG

1401 GGGGCGCTGG GCCTCGGGGT GGAGAGATGA GACCAAACTT TTGCGACGCG

1451 TACGAGCTGG GACTGACTCT GACGCACGTG CCCGGGAGCG TGCCTGCCAC

1501 GTGGGCCGGC GTAGGTCTGG AATCTCCAGA GGGACCGGGT GCCTTGGGCC

1551 GGGAAATGGC GGTATCGGCC CTAGTCGGAG TCCCGGCTGC GCTCGGATGT

1601 CTCCGCCCCG GCCTGGCAAG CCGATACGTG GTGGGCCCCG GAAGGTGGCT

1651 CTGCCGCGTG CCTTTTGCGC TGTGTTTCGG GCAAGAGGTG GTCCTGCCAG

1701 GTACCCCCAC GTGGCCGCAC CCGCCTCTTT AAGGGGCGGG GTAGTGCTGG

1751 GGAAAGGCAT AAGCTTCATG AGAAAATAAG GTAGTATTTT TAAGTGCCTT

1801 AATGATCTTC ACCGTTAATT TGATTCAAAT AAGGGTGGTA GATAAAGTAC

1851 CGGGATTTGT AGTATAAAAA CACGGTTGTG CTTAACTAAG GTAACGGGAG

1901 GAGAAATCAT TTCCTCAGGT TGACTTTTTA CCTTAGGGCA GGTTTTCTGT

1951 TGGTAAAGCC TGGGAGGAAA AATGTGGGCG GTTGAGAAGT AGTCCCTCTT

2001 GCATTGCCAT CAGGAGTAGT TTCTATGTTA GTTGTGGTGT TTGGCACTAT

2051 GAGAAATGAT CTGAGACGGA GATGATGGCG TATGAACACT AATGGCAAAA

2101 TATGAATGGC CTGAAATGTC GAGGTGGAGG TGTAATGATC TATTTGTGTC

2151 CATTTTAGGC AGGTAAAAAT CAAGGTGACC CCAAGAAAAT GGCTCCTCCT

2201 CCAAAGGAGG TAGAAGAAGA TAGTGAAGAT GAGGAAATGT CAGAAGATGA

FIG. 49 (CONT. 2)

2251   AGAAGATGAT AGCAGTGGAG AAGAGGTAAT TTTATCCAAC TTAATGCAGA

2301   ATTATGTTAA AACTACAAAA TGGAGAGTTA AGACATGAAA TTGGATATCT

2351   GTGGCAAAAA TAAGATTTTA TCAGGTATGT CTTATTGTAG TGGTTGAGTG

2401   TTTCACAAGC TCTTCATTGA CATGTCAAGA TGTCATTTGG CTAGTATTTG

2451   AATGTGAGTG CTAAGACGAG ACTGGGAATT TCTTTTACAT GTTCCTCTGC

2501   AGGGCTTGGA GTGTGATTTG TTGTGTTAAA TCATTACATT TTTCCAGTTT

2551   CAACATGTTA GCTCACCCCC ACATGTAGAG CTGGGCATTG TATTCAGAGC

2601   TGAGAATAAC CTTACCAGAT TCCTTTCCTA TCCTCCGAAT TAAAATTAAT

2651   TGGTCTCCAT TCCATATATA TATAACTGTA TCACTACTGG TTAAGTACTC

2701   GGGTGTAGAC TGAGGGCTGC CACCTCTCTT TGGTACCATT GACCCTCTTT

2751   AGCCACCTCC TGGCCTTTTA TTTGCCTCCA CTATAAAGAC AGCTGAGCAC

2801   TGAATTGTGC TCAGGTTTTC GTTGAGAACC TGAATGAAAG TTTTACTCTC

2851   CACACATTGC CTTGATAAAA CTACGGGATT TTAATGTAGC TAAATGATGA

2901   CTTTTATCAA ACTACCATGC ACACTCTTTG ATGTGTGATA GTTTTGTAAG

2951   GAATATTTAT ATTTAGCCTA TTCATTTTTT GTCTCAGGTC CTAAGAATTG

3001   AGCTTCACTG GGCTTGGTGG ACCGCAACCA CGAGGGCCCC AATGATTTAA

3051   TAAGTTAATG CTTGGAGCCT CCTATGTGTA ACGTTCTGAA TAATTTACAC

3101   ATAGCAATTC ATGACCTTAA ACATGTAAGG ATGATACTAT TACCATTTTC

FIG. 49 (CONT. 3)

3151 AGATGAGAAA GTTGGGGCTT GGGAAAGTAT GAGGTGTAAG AATTCAGAGG

3201 GTCTGGTTCA GAGGTATTTT CAGTGTTCAA AAGAGTTCCT TATGTCTGGG

3251 TATTCACCTT ATTATAGGGG CTCTGACTTA AGACAACATA ACAGAAGCCT

3301 GGAGTTTTAA CATGTCATAT GTGTCATGCG TATGTCTTGA ACCAGAGGCA

3351 TTGCCAGAGT CTAACAACTC ATTGGGACCA TGGTTATCTT TTTGGGTGTG

3401 GGGCTGGACT TACTGGTTTG GTTTTCATTT ATCTCAAGGT CGTCATACCT

3451 CAGAAGAAAG GCAAGAAGGC TGCTGCAACC TCAGCAAAGA AGGTGGTCGT

3501 TTCCCCAACA AAAAGGTTG CAGTTGCCAC ACCAGCCAAG AAAGCAGCTG

3551 TCACTCCAGG CAAAAAGGCA GCAGCAACAC CTGCCAAGAA GACAGTTACA

3601 CCAGCCAAAG CAGTTACCAC ACCTGGCAAG AAGGGAGCCA CACCAGGCAA

3651 AGCATTGGTA GCAACTCCTG GTAAGAAGGG TGCTGCCATC CCAGCCAAGG

3701 GGGCAAAGAA TGGCAAGAAT GCCAAGAAGG AAGACAGTGA TGAAGAGGAG

3751 GATGATGACA GTGAGGAGGA TGAGGAGGAT GACGAGGACG AGGATGAGGA

3801 TGAAGATGAA ATTGAACCAG CAGCGATGAA AGCAGCAGCT GCTGCCCCTG

3851 CCTCAGAGGA TGAGGACGAT GAGGATGACG AAGATGATGA GGATGACGAT

3901 GACGATGAGG AAGATGGTAA GGAGTTGTCT TGGTAGTTAC TGGGCTTCTG

3951 ATTACAAGGT ATCTTGAGAT TCTGGGATCA CATATTCCTT CATCGTACAA

4001 CCTGGAGATG AGATTAGAAT CTTGTGGGAA TTCTCTTGGG TTGTTGTGGT

FIG. 49 (CONT. 4)

4051 GTGCTAGACT TAATTACCCA TGAATGATTT TGTCCTCTTG AGAAAATTTC

4101 AATAGCACAT CTATTAGTGT TTTTTATAAT GTAGGATTTT CGTTTCTAAG

4151 TGATTTTTTT TTTTTTTTAA ATTTTTTTGA GATGGAGCTT TTGCTGTTTC

4201 CCAGGCGGGA GTGCAATGGC GCGCTATCTC GGCGCACTGC AGCCTCCATC

4251 TCCTGGGTTC AAGCAGTTCT GCCTCAGCCT CCCGAGTAGC GGGATTACAG

4301 GTGCCCACCA CCACACCCTA CTAATTTTGT ATTTTAGTAG AGACGACATT

4351 TCACCATGTT GGCCAGGCTG GCTCTGAACT TTGACCTCAG GTGATCCACC

4401 CACCTTAGGC TCTCCCAAAG TGCTAGGATT ACAGGTGAGA TATGCTGCGC

4451 CCGGCCCCAA GTGATCTATT CTTGCCATGA CTGTTAACTA AACATGGTGA

4501 CAGGATTCGA TTTTCTTTAC ATTAGATTTG AAAACCGATG TTGGTTTTGG

4551 GAGATTGCTG CAATTTTTAG GTGACTTCTC TTTCAGACTC TGAAGAAGAA

4601 GCTATGGAGA CTACACCAGC CAAAGGAAAG AAAGCTGCAA AAGTTGTTCC

4651 TGTGAAAGCC AAGAACGTGG CTGAGGATGA AGATGAAGAA GAGGATGATG

4701 AGGACGAGGA TGACGACGAC GACGAAGATG ATGAAGATGA TGATGATGAA

4751 GATGATGAGG AGGAGGAAGA AGAGGAGGAG GAAGGTACTT AAATTAGATT

4801 CTGACATACG ACATGAGTTA TGTTTAAAGG AGGCACTTAA GTGTTTGTGG

4851 CTACTGATGT GTGATACATT GTTTGACATC TTGTCCAGAG CCTGTCAAAG

4901 AAGCACCTGG AAAACGAAAG AAGGAAATGG CCAAACAGAA AGCAGCTCCT

FIG. 49 (CONT. 5)

4951   GAAGCCAAGA AACAGAAAGT GGAAGGTAAC TTGCAGAATT AGGGGATATG

5001   GGGGAGATAA ACAGCACAAA TGATGAATAA CAAAGGGACT TAATACTGAA

5051   ACCAGATGTT ACATTGTAGT GTGCTGATGT GCTGTGTATA GAAATTTTGC

5101   TTTGGAAACT AACTTTTTAC CACACTACAA GTAGACTGAG TTGAGCTTTT

5151   TTTGTGCAGG CACAGAACCG ACTACGGCTT TCAATCTCTT TGTTGGAAAC

5201   CTAAACTTTA ACAAATCTGC TCCTGAATTA AAAACTGGTA TCAGCGATGT

5251   TTTTGCTAAA AATGATCTTG CTGTTGTGGA TGTCAGAATT GGTATGACTA

5301   GGTAGCTGCT TCACTGCACG TTACATACCG TGGGTCTGTT AATTTTTCCT

5351   TCCCCTGTTA GCACAGTTAC TTTAGCCTGC CACTGTTAAA CATGAATACT

5401   GTAAACACTT CAAGGTTAGC ATTAGTGAAC TAAGTTAGAA TTAAACTGTA

5451   GATCCCCTAA GTTGCAATTT CCATAATCAG TCGTAACTTG GTATAGCACA

5501   GAATAATTTT TAGTAATTTT TTTGTTGTTT TTGTTATGTA TTGAGACGGA

5551   CGCTGGCTTT TGTTCAGGCT GGAGTACAGT GGCGCAATCT TGGCTCACTG

5601   CAACCTCTGC CTCCCGGGTT CAAGCGATTC TCCTGCCTAA CCTCCCAAGT

5651   GACTGGGATA CGGGTGCCAC TCACCATGCA TGGCTAATTT TTGTTTTGTA

5701   TTTAGTATCG ATTTCACCAT GTTGGTCGGC TGGTTTTGAA CTCCTGACCT

5751   CAAGTGATCC ACCCACCTCG GCCTCTCGAA GTGCTGGTAC AGCGTCACCA

5801   CCCTGCCAGT AAGTTTTAAT AATTTGGTGT TAGGTGGGAG AATGCTTGAA

FIG. 49 (CONT. 6)

5851 CCTGGGAGGC AGAGGTTGCA GTGAGCCAAG TTCGCGCCAC TGTACTCCAG

5901 CCTGGGCAAC AGATTGAGAC ACCGTCTCAA TTTAAAATAA TGTTTATTTT

5951 CTTGGAAGTA CCTTGAAACT ATTAGACCTG TCTAGTCATC ATAGTGAATA

6001 CTTTTATCCA GACAGGATTC TCCTGTATTA GTGCTTATAG GTGTTCTTTT

6051 GTCAGCTGCT ACTGTGAATT CTTATAAGCA ATTTAGCTCC ATGATGAAGA

6101 CCTCAAACGT GAATGTGCAT GTCATATCTT CATGCTGAGC CGTGTTCTGT

6151 AGCTGCAGTT TGCAGAGCCT TGACTTTGTT TTGCTATACT AGGGGTGCTT

6201 TTTAAAATGT GATCTTTGTT TGCACCATCA CATTTGTCTA GATACAGATT

6251 GTGATTTTGA TTTGTGTTTT CACCTGTTGT AATTTTGCCC TCCTCTCCAC

6301 CTGAAGGAAA TTTGGTTATG TGGATTTTGA ATCTGCTGAA GACCTGGAGA

6351 AAGCGTTGGA ACTCACTGGT TTGAAAGTCT TTGGCAATGA AATTAAACTA

6401 GAGAAACCAA AAGGAAAAGA CAGTAAGAAA GGTATGTAAG GCTTTATGAG

6451 TTATGCAATG AACTCAGGAG CTAGACTGCT AGGGAAAATG CTTTGTAACC

6501 CATTTCCCTT TGGTTTCCTC TTATTTTTTT TAAATCATTT TTTTCCTTTG

6551 GTTTCCTCTT AATGTGGGAA TTAAATGAGC TACAGTGTTT ACAAGGTACT

6601 TGGCACTGCT TGTCAGTGTA TAGGTAAATT CCTGAGTTAG GCAAGCAAGA

6651 GCACTCTTAT ACAGAACAAG AACCATTACA TGCACCTAAA TTAAGCTAAG

6701 GATCTTTCTT CACTGAAACT AGTTAGGTCC CTAATTACTC CCTATATACA

FIG. 49 (CONT. 7)

6751 GTGTAATGTT TTGAATTGGT ACATTCACTT TTTTTGTTAT GCGCGTCTAC

6801 TCTAGGTTGA ACTCCAGTGT ACCTAACAGA GAGTTTGACA TCAAGGCTGT

6851 GACAACATGG AGGGACCACT TGTGTGTTGA CACTGCTATA TCTCCATATT

6901 TAGCACCGAG CCTTGTACAT ATAGGATCTC AAATTATTTG TTGATAGAGC

6951 TATGTGTGTT TTTCCCCTCT TTTTGTTGTT GCCCCCCACC TTTGGTTTTT

7001 CAGGCCACAG AGCTCATTTT TGTTTTTTTA ATCTAGAGCG AGATGCGAGA

7051 ACACTTTTGG CTAAAAATCT CCCTTACAAA GTCACTCAGG ATGAATTGAA

7101 AGAAGTGTTT GAAGATGCTG CGGAGATCAG ATTAGTCAGC AAGGATGGGA

7151 AAAGTAAAGG GTATGTTCTT CTATTGAAAT GTAAGGGTTT TATTAACATT

7201 AATGCACTTC CTGCTTTATA AAAGAAATAT TGGTTTGATT TCCTTAGGCG

7251 TGTAACTTGG ACAGTTTAAC CTGTAAGTTT GTGCCTCAGT AACCCATCTG

7301 TACCATGGGG ATAATGTACT CATAGGGTGA TTTTAAAAGA CAAAGCTAAT

7351 ACTTACAAAG AAGCAAGTTT AATGCCTATC TTACATAAAT ACTTTGTAAG

7401 TAGTAGCAGT TCTTTCAGTG AGGTGAGGTT ACATGAAAAA ATTCCAAGTA

7451 TTTGTAAAAC TAGTGGGAAG TAAGAGGGAA GCTCGAGTTT TGATTGAAAA

7501 GTGGACTAAA CAAGGGCATT TTATGTACTC AGATCTGAAG CAAGTTCTGT

7551 GTTGCTGAGG TAAAAGCATT TGTGTTAATA TGGTTTTAAA AACCATGAGT

7601 TCTTCTCCCT CCATTGCAGG ATTGCTTATA TTGAATTTAA GACAGAAGCT

FIG. 49 (CONT. 8)

7651   GATGCAGAGA AAACCTTTGA AGAAAAGCAG GGAACAGAGA TCGATGGGCG

7701   ATCTATTTCC CTGTACTATA CTGGAGAGAA AGGTCAAAAT CAAGACTATA

7751   GAGGTGGAAA GAATAGCACT TGGAGTGGTA AGAAATTAGG CTTGTTCCAA

7801   GGTTTTCAGA ATTGGTTGAG GGAACTCTTC TAGTCTTTGT ATTTCATAAG

7851   TTTATAAATA CTTTTTAATC AAAGTTACTC AAATGTAGGT GAAGATCAAG

7901   GACATGATAC CCCAAGTCAT ACTCTTATTT GGAATAGTAA TTTCCAATCT

7951   TGAAATGAGA GCTCTAAATC ATTTTGCATT GGAATACAGT AGGCAAATCA

8001   AGCTTCCTTT GTAGGCATGT TTTATACTTT AAATGACTTG ACCATGTGCG

8051   TTTTGAACTC AGATGATTCT AGGAAAACAG ACCAGTCATC AGCCTATGTA

8101   AGAACAACCA GCAGGACATT GCAACACGTA CTAGGTACTT AATATGTTGA

8151   GTAACAGAAA TGGATTTAGC TTACGTCATG AGTATTTGTA TATAACTCAA

8201   GCACTGAAAT TCTTAGGGAA TAGATATTAC TGTTGTGACC GAAGCTGGGA

8251   CACTGTTTCA GAGTCTTAGG AATGTGGCTC TCTATTTCGA GGTGAATCAA

8301   AAACTCTGGT TTTAAGCAAC CTCTCCTACA GTGCAACAGA AGAAACTCTT

8351   CAGGAAGTAT TTGAGAAAGC AACTTTTATC AAAGTACCCC AGAACCAAAA

8401   TGGCAAATCT AAAGGGTAAG ATAATACCTT TGTATCATCA GTTATAGGCC

8451   TATATATGTC TTAGAGGTCT AAGGACGTAA GGTCATGTGT CCTGTAGAAA

8501   AAAGCTAAAT AATTTTAGCC TAGTAAATGA GTGTAAAATA AGTATATTTA

FIG. 49 (CONT. 9)

8551 GGTCCAACCT TGAGAGAAGG GCCTTGGCCA GATCATGTGA CCAGTGGTAT

8601 AGAGAGCATG TGCCTGGTAA ATTACTCTAA GCATTAACTG TTCATCCTCA

8651 GGTATGCATT TATAGAGTTT GCTTCATTCG AAGACGCTAA AGAAGCTTTA

8701 AATTCCTGTA ATAAAAGGGA AATTGAGGGC AGAGCAATCA GGCTGGAGTT

8751 GCAAGGACCC AGGGGATCAC CTAATGCCAG AAGCCGTAAG TTCACCTGGT

8801 TAGGGTGCTG TGGTTGGGGG TAGCACTCTC GGTGCTTTGT TTATTTTTGC

8851 ACAAATTCTG TGTTTCCTGT TCGCTACTGA GTGAACAATA ACTGGATATC

8901 GATGACTGAT TACCTGAGAA ATAATTGATG AAATCTCAAG AAAATTCCTC

8951 TAGATAGTCA AGTTCTGATC CAGCTGTCGT CAACTCAGAG TAGCAAGTTT

9001 GCCCATGATT TCCTGCCCCA TCCACTGGGC CCCACCTGCT TGGGTTGCTT

9051 TCCCACTTTC CATAGAAGAC TGGGGCAGGA TATCAACTAT GCAATGGCAA

9101 TTAAAAAATG TAAACCCAGA ATAGCCTTTA CTTTAATTAA GGACTAGTTG

9151 GCTTAGTTGC TTTTAACTGC TTTTTCACTA TAACAAGTAT CTTGGCTAGT

9201 AGTCATACTA GGCATTGTGC AAATTCAGTG TACGAACTGT GAATTCACAT

9251 AAATCGCAAA TTTTTTTTTC CTTCCCAGAG CCATCCAAAA CTCTGTTTGT

9301 CAAAGGCCTG TCTGAGGATA CCACTGAAGA GACATTAAAG GAGTCATTTG

9351 ACGGCTCCGT TCGGGCAAGG ATAGTTACTG ACCGGGAAAC TGGGTCCTCC

9401 AAAGGGTAAG GGAAGGAAGC GTGAGTGCTG CTTCCACTTG AAGGGGTTTT

FIG. 49 (CONT. 10)

9451 TGTTCTGTGC AGACCTTGAG TCTAATGTGT CTTCTCATTG AGCTCCTTCT

9501 GTCTATCAGT GGCAGTTTAT GGATTCGCAC GAGAAGAAGA GAGAATTCAC

9551 AGAACTAGCA TTATTTTACC TTCTGTCTTT ACAGAGGTAT ATTTAGCTGT

9601 ATTGTGAGAC ATTCTGGGGT TCAAGCTGTC ACACCAGTTA GTTTTCCATA

9651 GAGAGCTACT CTGCTGCACT GGTATCTTTT TCCCAAATAA ACAAGGCTAC

9701 TTCTGTGGGA TGGCTCCCCA GCATGTACAG TTAACTTGGG ACATGTGTAG

9751 TAGGTGCTTT TTATAATGGG CAATTTCATT TGGTGTTCTA GGTTTGGTTT

9801 TGTAGACTTC AACAGTGAGG AGGATGCCAA GGAGGCCATG GAAGACGGTG

9851 AAATTGATGG AAATAAAGTT ACCTTGGACT GGGCCAAACC TAAGGGTGAA

9901 GGTGGCTTCG GGGGTCGTGG TGGAGGCAGA GGCGGCTTTG GAGGACGAGG

9951 TGGTGGTAGA GGAGGCCGAG GAGGATTTGG TGGCAGAGGC CGGGGAGGCT

10001 TTGGAGGTAA GGCACGCAGA GATAATGACA CCACATAGCA TGTGCTCTTC

10051 AGACCCTGTG CCCTGTCACG GTTCCTAATC ACTGGGGAGG AGGAGCTTTG

10101 TACCCATTCT TTTAACAGTG TCTTGCCTTC CTCCTGTAGG GCGAGGAGGC

10151 TTCCGAGGAG GCAGAGGAGG AGGAGGTGAC CACAAGCCAC AAGGAAAGAA

10201 GACGAAGTTT GAATAGCTTC TGTCCCTCTG CTTTCCCTTT TCCATTTGAA

10251 AGAAAGGACT CTGGGGTTTT TACTGTTACC TGATCAATGA CAGAGCCTTC

10301 TGAGGACATT CCAAGACAGT ATACAGTCCT GTGGTCTCCT TGGAAATCCG

FIG. 49 (CONT. 11)

```
10351   TCTAGTTAAC ATTTCAAGGG CAATACCGTG TTGGTTTTGA CTGGATATTC

10401   ATATAAACTT TTTAAAGAGT TGAGTGATAG AGCTAACCCT TATCTGTAAG

10451   TTTTGAATTT ATATTGTTTC ATCCCATGTA CAAAACCATT TTTTCCTACA

10501   AATAGTTTGG GTTTTGTTGT TGTTACTTTT TTTTTTGTTT TTGTTTTTTT

10551   TTTTTTTGCG TTCGTGGGGT TGTAAAAGAA AAGAAAGCAG AATGTTTTAT

10601   CATGGTTTTT GCTTCACCGC TTTAGGACAA ATTAAAAGTC AACTCTGGTG

10651   CCAGACGTGT TACTTCCTAA AGAGTGTTTC CCCTGGAATC TCACTGGAGA

10701   GCATGGCAAA GCCAGCTCTG CCACTTGCTT CACCCATCCC AATGGAAATG

10751   GCTTAGTGCG TGTTTCCAGT ATCCCAGCCC TAACTAACTT GGTTGAAATG

10801   CTGGTGAGGG GACCTGCTCC TGCAGCCCTG GTGCTGACTT GAAGGCTGCT

10851   GCAGCTTCTC CTACTTTTAG CAGGTCTCGA GGATTATGTC TGAAGACCAC

10901   TCTGGAAAGA GGTCGAGGAA CAGATTAGTC AGGTTTCCTA GG
```

(SEQ ID NO: 24)

III.   "MEMGRRIHLELRNRTPSDVKELVLDNSRSNEGKLEGLTDEFEEL
EFLSTINVGLTSIANLPKLNKLKKLELSDNRVSGGLEVLAEKCPNLTHLNLSGNKIKD
LSTIEPLKKLENLKSLDLFNCEVTNLNDYRENVFKLLPQLTYLDGYDRDDKEAPDSDA
EGYVEGLDDEEEDEDEEEYDEDAQVVEDEEDEDEEEEGEEEDVSGEEEEDEEGYNDGE
VDDEEDEEELGEEERGQKRKREPEDEGEDDD"

III. (SEQ ID NO: 25)

1   GCTGGTTGAG CCTTCAAAGT CCTAAAACGC GCGGCCGTGG GTTCGGGGTT

FIG. 49 (CONT. 12)

```
51    TATTGATTGA ATTCCGCCGG CGCGGGAGCC TCTGCAGAGA GAGAGCGCGA

101   GAGATGGAGA TGGGCAGACG GATTCATTTA GAGCTGCGGA ACAGGACGCC

151   CTCTGATGTG AAAGAACTTG TCCTGGACAA CAGTCGGTCG AATGAAGGCA

201   AACTCGAAGG CCTCACAGAT GAATTTGAAG AACTGGAATT CTTAAGTACA

251   ATCAACGTAG GCCTCACCTC AATCGCAAAC TTACCAAAGT TAAACAAACT

301   TAAGAAGCTT GAACTAAGCG ATAACAGAGT CTCAGGGGGC CTGGAAGTAT

351   TGGCAGAAAA GTGTCCGAAC CTCACGCATC TAAATTTAAG TGGCAACAAA

401   ATTAAAGACC TCAGCACAAT AGAGCCACTG AAAAAGTTAG AAAACCTCAA

451   GAGCTTAGAC CTTTTCAATT GCGAGGTAAC CAACCTGAAC GACTACCGAG

501   AAAATGTGTT CAAGCTCCTC CCGCAACTCA CATATCTCGA CGGCTATGAC

551   CGGGACGACA AGGAGGCCCC TGACTCGGAT GCTGAGGGCT ACGTGGAGGG

601   CCTGGATGAT GAGGAGGAGG ATGAGGATGA GGAGGAGTAT GATGAAGATG

651   CTCAGGTAGT GGAAGACGAG GAGGACGAGG ATGAGGAGGA GGAAGGTGAA

701   GAGGAGGACG TGAGTGGAGA GGAGGAGGAG GATGAAGAAG GTTATAACGA

751   TGGAGAGGTA GATGACGAGG AAGATGAAGA AGAGCTTGGT GAAGAAGAAA

801   GGGGTCAGAA GCGAAAACGA GAACCTGAAG ATGAGGGAGA AGATGATGAC

851   TAAGTGGAAT AACCTATTTT GAAAAATTCC TATTGTGATT TGACTGTTTT

901   TACCCATATC CCCTCT
```

FIG. 49 (CONT. 13)

IV. (SEQ ID NO: 26)

"MSAPAAKVSKKELNSNHDGADETSEKEQQEAIEHIDEVQNEIDR
LNEQASEEILKVEQKYNKLRQPFFQKRSELIAKIPNFWVTTFVNHPQVSALLGEEDEE
ALHYLTRVEVTEFEDIKSGYRIDFYFDENPYFENKVLSKEFHLNESGDPSSKSTEIKW
KSGKDLTKRSSQTQNKASRKRQHEEPESFFTWFTDHSDAGADELGEVIKDDIWPNPLQ
YYLVPDMDDEEGEGEEDDDDDEEEEGLEDIDEEGDEDEGEEDEDDDEGEEGEEDEGED
D"

IV. (SEQ ID NO: 27)

```
  1   CGACCGCGGA GCAGCACCAT GTCGGCGCCG GCGGCCAAAG TCAGTAAAAA

 51   GGAGCTCAAC TCCAACCACG ACGGGGCCGA CGAGACCTCA GAAAAAGAAC

101   AGCAAGAAGC GATTGAACAC ATTGATGAAG TACAAAATGA AATAGACAGA

151   CTTAATGAAC AAGCCAGTGA GGAGATTTTG AAAGTAGAAC AGAAATATAA

201   CAAACTCCGC CAACCATTTT TTCAGAAGAG GTCAGAATTG ATCGCCAAAA

251   TCCCAAATTT TTGGGTAACA ACATTTGTCA ACCATCCACA AGTGTCTGCA

301   CTGCTTGGGG AGGAAGATGA AGAGGCACTG CATTATTTGA CCAGAGTTGA

351   AGTGACAGAA TTTGAAGATA TTAAATCAGG TTACAGAATA GATTTTTATT

401   TTGATGAAAA TCCTTACTTT GAAAATAAAG TTCTCTCCAA AGAATTTCAT

451   CTGAATGAGA GTGGTGATCC ATCTTCGAAG TCCACCGAAA TCAAATGGAA

501   ATCTGGAAAG GATTTGACGA AACGTTCGAG TCAAACGCAG AATAAAGCCA

551   GCAGGAAGAG GCAGCATGAG GAACCAGAGA GCTTCTTTAC CTGGTTTACT

601   GACCATTCTG ATGCAGGTGC TGATGAGTTA GGAGAGGTCA TCAAAGATGA
```

FIG. 49 (CONT. 14)

651   TATTTGGCCA AACCCATTAC AGTACTACTT GGTTCCCGAT ATGGATGATG

701   AAGAAGGAGA AGGAGAAGAA GATGATGATG ATGATGAAGA GGAGGAAGGA

751   TTAGAAGATA TTGACGAAGA AGGGGATGAG GATGAAGGTG AAGAAGATGA

801   AGATGATGAT GAAGGGGGAGG AAGGAGAGGA GGATGAAGGA GAAGATGACT

851   AAATAGAACA CTGATGGATT CCAACCTTCC TTTTTTTAAA TTTTCTCCAG

901   TCCCTGGGAG CAAGTTGCAG TCTT

V . (SEQ ID NO: 28)

CTTCGGTGTACGTGCTCCGGGATCTTCAGCACCCGCGGCCGCCATCGCCGTTGGCTTCTTCTGACTCATCTGCG
CCACTTGTCCGCTTCACACTCCGCGGCCGCCATCATGGTGAAGCTCGCGAAGGCAGGTAAAAATCAAGGTGACCCCAAGAAAA
TGGCTCCTCCTCCAAAGGAGGTAGAAGAAGATAGTGAAGATGAGGAAAATGTCAGAAGATGAGGAAGAGATGATAGCAGTGGA
GAAGAGGTCGTCATACCTCAGAAGAGAAAGGCAAGAGCAAGAGGCTGCTGCAACCTCAGCAAGAAGAGGTGGTCGTTTCCCAACAAA
AAAGGTTGCAGTTGCCACCAGCCAAGAAAAGCAGCTGTCACTCACTCAGCAAAAAGGCAGCAGCAACACTGCCAAGAAGA
CAGTTACACCAGCCAAGCAGTTACCACCACCTGGCAAGAAGGGAGCCACACCAGGGCAAAGCCAAAGCAAGAAGGAGCAACTCCTGGT
AAGAAGGGTGCTGCCATCCCAGCCAAGAAGAATGGCAAGAATGCCAAGAAGACAGTGATGAAGGAGGAGGA
TGATGACAGTGAGGAGGAGGATGAGGAGGATGAGGAGGATGAGGAGGAATTGAACCAGCCAGCAGCGATGAAAG

FIG. 49 (CONT. 15)

CAGCAGCTGCTGCCCCTGCCTCAGAGGATGAGGACGATGAGGATGATGAGGATGACGATGAGGAA

GATGACTCTGAAGAGAAGCTATGAGACTACACCAGCCAAAGGAAAGAAAGCTGCAAAAGTTGTTCCTGTGAAAGCCAA

GAACGTGGCTGAGGATGAAGAAGATGAGGAGGAGAAGAGAGGAAGAGAGCCTGTCAAGAAGCACCTGGAAAACGAAAGAAGGAA

ATGATGAAGAGATGAGGAGGAGAAGAGAGGAAGAGAGAGCCTGTCAAGAAGCACCTGGAAAACGAAAGAAGGAA

ATGGCCAAACAGAAAGCAGCTCCTGAAGCCAAGAAACAGAAAGTGAAGGCCACAGAACCGACTACGGCTTTCAATCTCTT

TGTTGGAAACCTAAACTTAACAAATCTGCTCCTGAATTAAAAACTGGTATCAGCGATGTTTTTGCTAAAAATGATCTTG

CTGTTGTGGATGTCAGAATTGGTATGACTAGGAAATTTGGTTATGTGGATTTTGAATCTGCTGAAGACCTGGAGAAAGCG

TTGGAACTCACTGGTTTGAAAGTCTTTGGCAATGAAATTAAACTAGAGAAACCAAAAGGAAAAGACCAGTAAGAAAGAGCG

AGATGCCGAACACTTTTGGCTAAAAATCTCCCTTACAAAGTCACTCAGGATGAATTGAAAGAAGTGTTTGAAGATGCTG

CGGAGATCAGATTAGTCAGCAAGGATGGGAAAAGTAAAGTTGCTTATATTGAATTAAGACAGAAGCTGATGCAGAG

AAAAAACCTTTGAAGAAAGCAGGGAACACAGAGATCGATGGGGCGATCTATTCCCTGTACTATACTGGAGAAAGTCAAAA

TCAAGACTATAGAGGTGGAAAGAATAGCACTTGGAGTGGTGAATCAAAAACTCTGGTTTAAGCAACCTCTCCTACAGTG

CAACAGAAGAAACTCTTCAGGAAGTATTTGAGAAGAAGCAACTTTATCAAAGTACCCCAGAACCAAAATGGCAAATCTAAA

GGGTATGCATTTATAGAGTTTGCTTCATTCGGAAGAACGCTAAAGAAGCTTAAATTCCTGTAATAAAAGGAAATTGAGGG

CAGAGCAATCAGGCTGGAGTTGCAAGGATGTCAAGGGGATCACCTAATGCCAGAAGCCAGCCATCCAAAACTCTGTTGTCA

AAGGCCTGCTGCTGAGGATACCACCTGAAGAGACATTAAAGGAGTCATTGACGGCTCCGTTCGGGGCAAGGATAGTTACTGAC

CGGGGAAACTGGGTCCTCCAAAGGGTTGGTTTGTAGACTTCAACAGTGAGGAGGATGCCAGAGGAGGCCATGGAAGACGG

TGAAATTGATGGAAATAAAGTTACCTTGGACTGGGCCCAAACCTAAGGGTGAAGGTGGCTTCGGGGGTCGTGGTGGAGGCA

GAGGCGGCTTTGGGAGGACGCGAGGTGGTGTAGGAGGCCGGAGGGCGGGATTGGTGGCAGAGGGCCGGGGAGGCTTTGGAGGG

CGAGGAGGCTTCCGAGGAGGCAGAGGAGGAGGAGGTGACCACAAGCCACAAGGAAAGAGACGAAGTTGAATAGCTTCT

GTCCCTCTGCTTTCCCTTTCCATTTGAAAGAAAGGACTCTGGGGTTTTACCTGTTACTGATCAATGACAGAGCCTTCT

GAGGACATTCCAAGACAGTATACAGTCCTGTGGTCTCCTTGGAAATCCGTCCAGTTAACATTCAAGGCCAATACCGTGT

TGGTTTTGACTGATATTCATATAAACTTTTAAAGAGTTGAGTGATGAGCTAACCCTTATCTGTAAGTTTTGAATTTA

TATTGTTCATCCCATGTACAAAACCATTTTCCTAC